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GenCore version 5.1.3

OM protein - nucleic search, using frame_plus_p2n model

Run on:

November 9, 2002, 07:32:20 ; Search time 2740 seconds

(without alignments)
2018.078 Million cell updates/secTitle:
Perfect score: US-09-895-298A-83

Sequence: 1 MMNFQPPSKAWRASQMMFF RDGSDLRSRSVQEGNPR A 190

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Word size: 4

Total number of hits satisfying chosen parameters: 2253933

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL:frame+_P2n.model -DEV=xlp
-O=/cgn2_1/USPRO_spool/US0985298/runat_06112002_160752_3565/app_query.fasta_1..327
-DB=GenEmbl -FORMAT=fasta -SUPPRX=oligna_rge -MINMATCH=0.1 -LOOCT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human&0.col -LIST=45
-DOCALIGN=200 -THR SCORE=500 -THR MIN=4 -ALIGN=15 -MOD=LOCAL -OUTFORMAT=Pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US0985298 -ERUNID=erunat_06112002_160752_3565 -NCPU=6 -TCPU=3
-NO_XLPPY -NO_NMAP -LARGEQUERY -NEGSCORES=0 -WAIT -LONGLOG -DEV - TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7 -DELEXT=7

Database : Genbank:*

1: gb_bai:*

2: gb_htg:*

3: gb_in:*

4: gb_on:*

5: gb_cv:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Query	Description
1	190	100.0	1219	6	AX108540	AX108540 Sequence	AK023655 Homo sapi
2	190	100.0	1813	9	AK023655		AK108558 Sequence
3	190	100.0	1960	6	AX108538		AX108534 Sequence
4	190	100.0	2407	6	AX108534		AX108536 Sequence
5	190	100.0	2521	9	BCC27602		BC027602 Homo sapi
6	190	100.0	2760	9	AK093944		AK093944 Homo sapi
7	135	71.1	2387	9	AK097718		AK097718 Homo sapi
8	126	66.3	2399	9	HU91321		U91321 Human Chrom
9	59	31.1	220633	2	AC130456		AC130456 Homo sapi
10	59	31.1	223380	2	AC130456		AC003108 Human Chr
11	35	18.4	164564	9	HDAC003108		Contamination (3 of
12	25	13.2	110000	2	AC124441		AJ297000 Mus muscu
13	18	9.5	623	10	MMC297000		AC108717 Mus muscu
14	17	8.9	71596	2	AC10877		AX071021 Sequence
15	16	8.7	4012	6	AK071021		AC10877 Mus muscu
16	12	6.3	71596	2	AC10877		AC10877 Mus muscu
17	10	5.3	4790	1	STVARABAD		M11047 S. typhimuri
18	10	5.3	4790	1	AEO08698		AEO08698 Salmonell
19	10	5.3	91692	2	CNS08C9G		AL732641 Oryza sat
20	10	5.3	150789	9	HS21F7		AL033375 Human DNA
21	10	5.3	150789	2	AC094128		AC094128 Rattus no
22	10	5.3	170372	2	AC109276		AC109276 Mus muscu
23	10	5.3	190000	9	AF213884		AF213884 Homo sapi
24	10	5.3	199880	9	AC021120		AC021120 Homo sapi
25	9	4.7	3310	6	AX135333		AX135333 Sequence
26	9	4.7	1534	1	ERFU94356		U94356 Enterococcus
27	9	4.7	1949	8	ARORAH		L38835 Arachis hyp
28	9	4.7	1949	1	AE011768		AE011768 Xanthomon
29	9	4.7	1949	1	U00064		U00064 Caenorhabdi
30	9	4.7	76967	9	AC008475		AC008475 Homo sapi
31	9	4.7	88065	9	AP002015		AP002015 Homo sapi
32	9	4.7	98065	8	ATP14P22		AL137082 Arabidops
33	9	4.7	98239	8	ATP14P22		AC104655 Homo sapi
34	9	4.7	99304	9	AC106825		AC106825 Homo sapi
35	9	4.7	107397	2	AP00612		AP00612 Homo sapi
36	9	4.7	110440	2	HS293E14		282169 Homo sapi
37	9	4.7	110441	2	HS23		AC094341 Rattus no
38	9	4.7	113116	2	AC094341		AC104655 Homo sapi
39	9	4.7	115832	2	AC099324		AC099324 Oryza sat
40	9	4.7	116758	2	AP004134		AP004134 Oryza sat
41	9	4.7	120126	2	AC087096		AC087096 Oryza sat
42	9	4.7	122167	2	AP005302		AP005302 Oryza sat
43	9	4.7	122288	9	AL359384		AL359384 Human DNA
44	9	4.7	123620	9	AC103891		AC103891 Oryza sat
45	9	4.7	126582	9	AC010241		AC010241 Homo sapi

ALIGNMENTS

Db 511 ARCTCTTGCTTTCCATCCCTACGGGCTTGTGACCCCTGGCCATCACCAC 570
 Qy 41 TPargLeuLysProSerAlaAspCysGlyProPheArgLeuProPheLeuHis 60
 Db 571 TGGAGATTGAGCCCTACGTACTGTCGCCCTTGAGGTCTGCCTCTTCATTC 630
 Qy 61 SerIleTrpSerTrpIleAspThrLeuSerThrArgProGlyTrpLeuTrpValTrp 80
 Db 631 TCCATCTACGCGATCACACCTAATCATGGCCCTGCTACTGAGGTTGG 690
 Qy 81 IleTrpArgAsnLeuIleGlySerValHisPhePhePheThrArgProGlyTrpLeuTrpValTrp 100
 Db 691 ATCTATCGGGACCCATGGAGTGCCTCTTCATTCACCCAGGATGTGCTA 750
 Qy 101 IleLeuThrTyroLeuTrpGlnIleThrGluGlyArgIleMetIleArgLeu 120
 Db 751 ATCATCACCTATCTTACGGAGATCACAGAGGAGGAAATGATAGCTGC 810
 Qy 121 HisGluGlnIleAsnGluGlyLysAspLysMetPheLeuIleGluIleLeuIle 140
 Db 811 CATGCGCATCATRATAGGGCAAGATAATGTTGATAGAAATGATGTCAG 870
 Qy 141 LeuGlnAspMetGluLysAsnProSerSerLeuValLeuGluArgGluVal 160
 Db 871 CTGCAAGGATATGGAGAACGAAACCCAGCTACTGTCAGAACAGAGAGGTG 930
 Qy 161 GluGlnGlnGlyPheLeuIleGluGlyLysAspLysMetPheLeuIleGluIleLeuIle 180
 Db 931 GACGAAACAGGCTTGTGATTTGGGGACATGATGGCAGTCTGACTTGCGATCTGA 990
 Qy 181 ArgSerValGlnGluGlyAsnProArgAla 190
 Db 991 AGATCGAGTCAGAGGATTCAGGCC 1020

RESULT 3
 AX108538

LOCUS AX108538 1960 bp DNA linear PAT 30-APR-2001
 DEFINITION Sequence 5 from Patent WO123417.
 ACCESSION AX108538
 VERSION AX108538.1 GI:13923838
 KEYWORDS human.
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 1960)
 AUTHORS vinyls Y de Bassols,C.
 TITLE Human tumor-associated lak-4p related polynucleotides and polypeptides and their uses
 JOURNAL Patent: WO 0123417-A 5 05-APR-2001;
 SMITHKLINE BEECHAM BIOLOGICALS S.A. (BB)
 FEATURES source
 /organism="Homo sapiens"
 1. 1960
 /db_xref="taxon:9606"
 BASE COUNT 515 a 439 c 447 g 559 t
 ORIGIN

Alignment Scores:
 Pred. No.: 3.54e-189 Length: 1960
 Score: 190.00 Matches: 190
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00%
 Query Match: 6 Gaps: 0
 DB: US-09-895-298A-83 (1-190) x AX108538 (1-1960)

Qy 1 MethMetAsnPheGlnProProSerLysAlaTrpArgLaserGlnMetMetThrPhePhe 20
 Db 745 ATGAGAAATTCCACGCTCGAGCAAGCCTGGGGCTACAGATGACTTCTC 804
 Qy 21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuCysThrLeuAlaIleThrIle 40

RESULT 4
 AX108534

LOCUS AX108534 2407 bp DNA linear PAT 30-APR-2001
 DEFINITION Sequence 1 from Patent WO123417.
 ACCESSION AX108534
 VERSION AX108534.1 GI:13923834
 KEYWORDS human.
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 2407)
 AUTHORS vinyls Y de Bassols,C.
 TITLE Human tumor-associated lak-4p related polynucleotides and polypeptides and their uses
 JOURNAL Patent: WO 0123417-A 1 05-APR-2001;
 SMITHKLINE BEECHAM BIOLOGICALS S.A. (BB)
 FEATURES source
 /organism="Homo sapiens"
 1. 2407
 /db_xref="taxon:9606"
 BASE COUNT 635 a 557 c 546 g 669 t
 ORIGIN

Alignment Scores:
 Pred. No.: 4.19e-189 Length: 2407
 Score: 190.00 Matches: 190
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00%
 Query Match: 100.00% Indels: 0
 DB: US-09-895-298A-83 (1-190) x AX108534 (1-2407)

Qy 1 MetMetAsnPheGlnProProSerLysAlaTrpArgLaserGlnMetMetThrPhePhe 20
 Db 1192 ATGATGATTTCAGCTCCGGAGCAAGCCCTGGCGGCCCTACAGATGACTTCTC 1251

QY 21 IlePhelLeupePhepheProSerPheThrGlyValLeucysThrIleuaIleThrile 40
Db 1252 ATCTCTTGCCTTCCTCCATCCCTCACGGGGGCTTGCGACCTGGCATCACCAC 1311
QY 41 TrpAgleulysproSerAlaAspCysGlyProphearglyLeuproLepheileHis 60
Db 1312 TGGAGATTGAGCCCTCAGCTGACTGTGAGCTTGAGGTCGCCCTTCGAGCTGCCCTCTCTTCAC 1371
QY 61 SerIleuysSerPhePheLeuAspPheIleSerThrArgProGlyTyroLeuIleValTrp 80
Db 1372 TCCCTCTACAGCTGATCACAACCTAAAGTACAGCACTGGCTTCGAGCTGCCCTCTCTTCAC 1431
QY 81 IleTyraGargAsnLeuIleIleGlySerValHisPhephePheIleThrLeuIleValLeu 100
Db 1432 ATCPATCGGACACCTCATGGAAAGTTGCACTCTTCATCCACCCCTCATGGCTA 1491
QY 101 IleLeuIleTyreLeuTyrrpGlnIleThgIleGlyArgLysIleMetIleArgLeuIle 120
Db 1492 ATCATCACCTATCTTACGGACATCACAGAGGAAGGAGATATGATAAGCGTC 1551
QY 121 HisGluGlnIleLeuAsnGluGlyLysAspLysMetPhepheLeuIleGlyuLeuIle 140
Db 1552 CAGGAGGATCATTAATGAGGCCAAAGATAAGATGAGGAGGAAATTCATGGCTA 1611
QY 141 LeuGlnAspMetGluLysAlaAsnProSerSerIeuAspLeuArgGluVal 160
Db 1612 CTGGAGGATATGGAGAGAACCCAGCTCAGCTGACTGTGCTGGAAAGGAGAGCTG 1671
QY 161 GluGlnGlyIleLeuIleAsnGluGlyArgLysIleMetIleArgLeuIle 170
Db 1672 GAGCAACAGGCTTTCGATTCGGGACATGATGCCAGCTGACTGGCGATCTAGA 1731
QY 181 ArgSerValGlnGluGlyAsnProArgIla 190
Db 1732 AGATCAGTCAGAGGAAATCCAAGGCC 1761

RESULT 5
LOCUS AX108536
DEFINITION AX108536 Sequence 3 from Patent WO0123417. DNA linear PAT 30-APR-2001
ACCESSION AX108536
VERSION 1.0
KEYWORDS SOURCE
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 2521)
AUTHORS vinyls Y de Bassols C.
TITLE Human tumor-associated lak-4p related polynucleotides and
Polypeptides and their uses
PATENT: WO 0123417-A 3 05-APR-2001;
JOURNAL SMITHKLINE BECHAM BIOLOGICALS S.A. (BE)
FEATURE source
1. /organism="Homo sapiens"
/organism="Homo sapiens"
/db:xref=taxon: 9606
ORIGIN 662 a 583 c 503 g 693 t

RESULT 6
LOCUS BC027602
DEFINITION BC027602 Human sapiens, Similar to RIKEN cDNA 493243L08 gene, clone MGC:26648 IMAGE:4839111, mRNA, complete cds.
ACCESSION BC027602
VERSION BC027602.1
KEYWORDS GCG.
SOURCE
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 2760)
AUTHORS STRAUBER,R.
TITLE Direct Submission
JOURNAL Submitted (08-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH MGC Project URL: http://mgc.nci.nih.gov
REMARK Contact: MGC help desk
COMMENT Email: crapsb-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Institute for Systems Biology
http://www.Systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
DB: US-09-895-298A-83 (1-190) x AX108536 (1-2521)

QY 1 MetMetAsnPheGlnProSerIysAlaTrpGalaSerGlnMetMetThrPhephe 20
Db 1306 ATGATGAATTCCACCTCGAGCAGAACCTGGCGGCCCTCACAGATGAGTCTTC 1365
This clone was selected for full length sequencing because it

passed the following selection criteria: GenomeScan gene prediction, Similarity but not identity to protein.

FEATURES

source

1. 2760
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MGC:26648 IMAGE:4839111"
/tissue_type="testis"
/clone lib="NIH MGC_97"
/lab_host="BII0B"
/note="vector: pbluescript"

CDS

213. 2495

</codon_start-1

/product="similar to RIKEN cDNA 4932443L08 gene"

/protein_id="AAH27602_1"

/translation="MLSDHHVNELLQVENVAVSVQSHPSSNQ1FQEVKVLDDINMV

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LNSISRAVRRSKNSLSELNSLWQKTLKIGKFGNSVLSTSFRMLMKNSF

LNFSEFLIIPQTVAKNLNTQSLWQKTLKIGKFGNSVLSTSFRMLMKNSF

NMQLAVITFTGACTTCTFFSLMSAKFRRNNITPHYTTGGITKLICWDFTVTHE

AYRKOKNLSSTEERNLSELRQNSKLUQNLTRFSAYMVANWVSGVIAACAVV

YLAEYNLEFLKHSNPQAVLWLFUVSCINLAQPCIVSMPLVERYEMPHREYVLL

RNLFLKSIIGLICYWINTVALSGEECWETLGQDTRILQFLDFVSLWSNIGEL

RRLIGMQLTSGLQEFDIARVNLIELAQTLWIGTTPCLPFIQMLMFIMYFK

LPLFHISTSYIWDLISRSPGYLAWWVTRNLIGSVHEFFLTILVLTIVLYMOTEG

RKJMRLRHLQEOLINEKGKMLKTEKLKLQDMERKANPSSLVLERVEQQFLHLGE

HOGDSLMSRSRSGNRNA"

BASE COUNT 739 a 637 c 625 g 759 t

ORIGIN

Alignment Scores:

Pred. No.: 4.69e-189 Length: 2760

Score: 190.00 Matches: 190

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indexes: 0

DB: 9 Gaps: 0

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QY 1 MetMetAsnPheGlnProProSerlysAlaTrpArgAlaSerGlnMetMetThrPhephe 20
 Db 1025 ATGATGATTTCAGCCAGCTCCAGCAAGCCCTGGGGCCTCGCATGATGACTTC 1084
 QY 21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuCystInLeuAlaIleThrile 40
 Db 1085 ATCTTCCTGCCTTCTTCCATCCCTCACGGGCTCTGACCCCTGGCATAACCAC 1144

QY 41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheHis 60
 Db 1145 TGGAGATTCAGCCCTACCTGACTGTCGCCCTTGAGGTCTGGCCCTCTCATC 1204
 QY 61 SerIleTyrsTerPheLeuPheLeuSerThrArgProGlyLeuLeuPheValIrp 80
 Db 1205 TCCATCTACAGCTGATCGACACCCCTAACTGACAGGCCCTGGCCTACCTGGTTGG 1264

QY 81 IleTyrsArgAsnLeuIleLeuIleSerValHisPhePhePheLeuLeuLeuLeu 100
 Db 1265 ATCTACCGAACCTCATCTGGAAGTGTGACTCTTTCATCCCTACCTCATGTC 1324

QY 101 IleLeuThrTyreLeuTyrrPheGlnIleThrGluGlyArgLysIleMetIleArgLeu 120
 Db 1325 ATCATCACCTATCTTACTGGGATCACAGGGGAGGATATGATAAGGCTGCT 1384

QY 121 HisGluGlnIleLeuAsnGluGlyLysAspLysMetIleLeuLeuGlu-LysLeuIle 140
 Db 1385 CTGGAGCAGATCATTAATGAGGCAAGATAAATGTCCTGATAGG-AAATTGATCAA 1443

QY 140 SteugIuAspMetGluLysLysAlaAsnProSerSerLeuLeuLeuGluGluGlu 160
 Db 1444 GCTGCAAGATATGGAGAGAAGAACCCAGCCTACTGTCGAAAGGAGAGGT 1503

QY 160 IGLuGlnGlnGlyPheLeuHisLeuGlyLysIleAspGlySerIleAspIleAspSer 180
 Db 1504 GGAGCACAAGGCTTGTGATTTGGGGACATGTTGGAGCTTGCGAGCT 1563

QY 180 GARGGAAValGlnGluGlyAsnProArgAla 190
 Db 1564 AAGATCAGTCAGAGGATATCCAGGGCC 1594

RESULT 8
 Locus AK097718
 Definition Homo sapiens 2399 bp mRNA linear PRI 15-JUL-2002
 Accession AK097718
 Version 1
 Keywords oligo capping; fis (full insert sequence); clone; clone:TEST12037081.

Organism Homo sapiens
 Reference 1
 Authors Oshima,A., Takahashi-Fuji,A., Tadae,T., Imose,N., Takuchi,K., Arita,M., Matsuhashi,K., Yuki,H., Hara,H., Sugiwama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hiro,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sakine,M., Kikuchi,H., Kanda,K., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
 Title NEDO human cDNA sequencing project
 Journal Unpublished

REFERENCE 2 (bases 1 to 2399)
 AUTHORS Isogai,T. and Yamamoto,J.
 TITLE Direct Submission
 JOURNAL Submitted (04-JUL-2002). Takao Isogai, FLJ Project(HRI Team); 2-6-7 Kazusa-Kanamori, Kisarazu, Chiba 292-0812, Japan
 COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library

construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'-&3'-end one pass sequencing: RAB, Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
 Location: (Qualifiers
 source 1. 2399
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="TEST12037081"
 /tissue_type="testis"
 /clone_lib="TEST12"
 /note="cloning vector: pME18SFL3"

BASE COUNT

610 a 591 c 528 g 670 t
 ORIGIN

Alignment Scores:

Pred. No.: 5.37e-122 Length: 2399
 Score: 126.00 Matches: 126
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 66.328 Indels: 0
 DB: 9

US-09-895-298a-83 (1-190) x AK097718 (1-2399)

QY 1 MetMetAsnPheGlnProProSerlysAlaTrpArgAlaSerGlnMetMetThrPhe 20
 Db 1933 ATGATGATTTCAGCCAGCAGCAAGCCCTGGCGGCTTCAGAGTATGACTTC 1992

QY 21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuCysThrLeuAlaIleThrile 40
 Db 1993 ATCTTCCTGCCTTTCCTGGCCATCCACCGGGCTTGACCCATGGCCATCAC 2052

QY 41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheHis 60
 Db 2053 TGGAGATTTGAGCTCTTACGGACTGTCGACTGTCGCCCTTGAGGCTGCTGCCTCTCATCAC 2112

QY 61 SerIleTyrsTerPheLeuPheLeuSerThrLeuSerThrArgProGlyLeuLeuPheValIrp 80
 Db 2113 TCCATCTACAGCTGGATCAGACCCCTAGTACACGGCTGCTACCTGTCGGTCTGG 2172

QY 81 IleTyrsArgAsnLeuIleGlySerValHisPhePhePheLeuLeuLeuLeu 100
 Db 2173 ATCTTCGGACCTGATGGAGCTTCACCGAGTCGACTCTTCCTCCACCTCATGCT 2232

QY 101 IleLeuThrTyreLeuTyrrPheGlnIleThrGluGlyArgLysIleMetIleArgLeu 120
 Db 2233 ATCATCACCTTACTGGAGCTCACAGAGGAGGATATTGATAAGGCTGCT 2292

QY 121 HisGluGlnIleLeuAsn 126
 Db 2293 CATGGAGCAGATCATTAAT 2310

RESULT 9
 Locus HU091321
 Definition Human Chromosome 16 BAC clone C1T987SK-A-363E6, complete sequence.
 Accession U91321
 Version U91321.1
 HGNC 1. GI:2951946
 Keywords
 Organism Homo sapiens

Bukarjota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 220633)
 Loftus,B.J., Kim,U.J., Shedd, V.P., Kalush,F., Brandon,R., Fuhrmann,J., Mason,T., Crosby,M.L., Barstread,M., Cronin,L., Deslattes,Mays,A., Cao,Y., Xu,R.X., Kang,H.L., Mitchell,S., Eichler,E.E., Harris,P.C., Venter,J.C., and Adams,M.D., from human chromosomes and other features in 12 Mb of DNA sequence Genomics 60 (3), 295-308 (1999)

			ORGANISM	Mus musculus
			REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1	Tolstogon, G. V., Mothes, E., Shoeman, R. L. and Traub, P.		AUTHORS	
	Isolation of SDS Stable Complexes of the Intermediate Filament Protein Vimentin with Repetitive, Mobile, Nuclear Matrix Attachment Region, and Mitochondrial DNA Sequence Elements from Cultured Mouse and Human Fibroblasts		JOURNAL	Cell Biol. 20 (9), 531-554 (2001)
	11747605		PUBMED	(2 bases 1 to 623)
	Tolstogon, G. V.		REFERENCE	
	Direct Submission		AUTHORS	
	Submitted (04-SEP-2000) Tolstogon G.V., Max-Planck-Institut fuer Zellbiologie, Rosenthal, Laedenburg/Heidelberg 68526, Germany		JOURNAL	
			FEATURES	Location/Qualifiers
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				repeat_region 346..623 /rpt_family="H4R"
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			Alignment Scores:	
			Pred. No.:	3..15e-09
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			Percent Similarity:	Matches: 18
			Best Local Similarity:	Conservative: 0
			Query Match:	Mismatches: 0
				Indels: 0
				Gaps: 0
			RESULT 14	
			AC12444_2/c	
			WPCOMMENT	
			Sequence split into 5 fragments	LOCUS AC12444 Accession AC12444
			Fragment Name	Begin End
	AC12444_0			110000 1
	AC12444_1			100001 210000
	AC12444_2			310000 410000
	AC12444_3			300001 400001
	AC12444_4			410492
			Continuation (3 of 5) of AC12444 from base 200001 (AC12444 Mus musculus chromosome UNK	
			Alignment Scores:	
			Pred. No.:	9..89e-15
			Score:	Length: 110000
			Percent Similarity:	Matches: 25
			Best Local Similarity:	Conservative: 0
			Query Match:	Mismatches: 0
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				Gaps: 0
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				ORIGIN
				Alignment Scores:
			Pred. No.:	25..9.89e-15
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			Best Local Similarity:	Conservative: 0
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				Indels: 0
				Gaps: 0
			US-09-895-298A-83 (1-190) x MMU297000 (1-623)	
				BASE COUNT 140 a 157 c 167 g 159 t
				ORIGIN
				Alignment Scores:
			Pred. No.:	25..9.89e-15
			Score:	Length: 110000
			Percent Similarity:	Matches: 25
			Best Local Similarity:	Conservative: 0
			Query Match:	Mismatches: 0
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				Gaps: 0
			US-09-895-298A-83 (1-190) x MMU297000 (1-623)	
				BASE COUNT 140 a 157 c 167 g 159 t
				ORIGIN
				Alignment Scores:
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				Gaps: 0
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				BASE COUNT 140 a 157 c 167 g 159 t
				ORIGIN
				Alignment Scores:
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			Score:	Length: 110000
			Percent Similarity:	Matches: 25
			Best Local Similarity:	Conservative: 0
			Query Match:	Mismatches: 0
				Indels: 0
				Gaps: 0
			US-09-895-298A-83 (1-190) x MMU297000 (1-623)	
				BASE COUNT 140 a 157 c 167 g 159 t
				ORIGIN
				Alignment Scores:
			Pred. No.:	25..9.89e-15
			Score:	Length: 110000
			Percent Similarity:	Matches: 25
			Best Local Similarity:	Conservative: 0
			Query Match:	Mismatches: 0
				Indels: 0
				Gaps: 0
			US-09-895-298A-83 (1-190) x MMU297000 (1-623)	
				BASE COUNT 140 a 157 c 167 g 159 t
				ORIGIN
				Alignment Scores:
			Pred. No.:	25..9.89e-15
			Score:	Length: 110000
			Percent Similarity:	Matches: 25
			Best Local Similarity:	Conservative: 0
			Query Match:	Mismatches: 0
				Indels: 0
				Gaps: 0
			US-09-895-298A-83 (1-190) x MMU297000 (1-623)	
				BASE COUNT 140 a 157 c 167 g 159 t
				ORIGIN
				Alignment Scores:
			Pred. No.:	25..9.89e-15
			Score:	Length: 110000
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				Gaps: 0
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				BASE COUNT 140 a 157 c 167 g 159 t
				ORIGIN
				Alignment Scores:
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				Gaps: 0
			US-09-895-298A-83 (1-190) x MMU297000 (1-623)	
				BASE COUNT 140 a 157 c 167 g 159 t
				ORIGIN
				Alignment Scores:
			Pred. No.:	25..9.89e-15
			Score:	Length: 110000
			Percent Similarity:	Matches: 25
			Best Local Similarity:	Conservative: 0
			Query Match:	Mismatches: 0
				Indels: 0
				Gaps: 0
			US-09-895-298A-83 (1-190) x MMU297000 (1-623)	
				BASE COUNT 140 a 157 c 167 g 159 t
				ORIGIN
				Alignment Scores:
			Pred. No.:	25..9.89e-15
			Score:	Length: 110000
			Percent Similarity:	Matches: 25
			Best Local Similarity:	Conservative: 0
			Query Match:	Mismatches: 0
				Indels: 0
				Gaps: 0
			US-09-895-298A-83 (1-190) x MMU297000 (1-623)	
				BASE COUNT 140 a 157 c 167 g 159 t
				ORIGIN
				Alignment Scores:
			Pred. No.:	25..9.89e-15
			Score:	Length: 110000
			Percent Similarity:	Matches: 25
			Best Local Similarity:	Conservative: 0
			Query Match:	Mismatches: 0
				Indels: 0
				Gaps: 0
			US-09-895-298A-83 (1-190) x MMU297000 (1-623)	
				BASE COUNT 140 a 157 c 167 g 159 t
				ORIGIN
				Alignment Scores:
			Pred. No.:	25..9.89e-15
			Score:	Length: 110000
			Percent Similarity:	Matches: 25
			Best Local Similarity:	Conservative: 0
			Query Match:	Mismatches: 0
				Indels: 0
				Gaps: 0
			US-09-895-298A-83 (1-190) x MMU297000 (1-623)	
				BASE COUNT 140 a 157 c 167 g 159 t
				ORIGIN
				Alignment Scores:
			Pred. No.:	25..9.89e-15
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				BASE COUNT 140 a 157 c 167 g 159 t
				ORIGIN
				Alignment Scores:
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				BASE COUNT 140 a 157 c 167 g 159 t
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				Alignment Scores:
			Pred. No.:	25..9.89e-15
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			Percent Similarity:	Matches: 25
			Best Local Similarity:	Conservative: 0
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				Gaps: 0
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				Alignment Scores:
			Pred. No.:	25..9.89e-15
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				BASE COUNT 140 a 157 c 167 g 159 t
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				Alignment Scores:
			Pred. No.:	25..9.89e-15
			Score:	Length: 110000
			Percent Similarity:	Matches: 25
			Best Local Similarity:	Conservative: 0
			Query Match:	Mismatches: 0
				Indels: 0
				Gaps: 0
			US-09-895-298A-83 (1-190) x MMU297000 (1-623)	
				BASE COUNT 140 a 157 c 167 g 159 t
				ORIGIN
				Alignment Scores:
			Pred. No.:	25..9.89e-15
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				BASE COUNT 140 a 157 c 167 g 159 t
				ORIGIN
				Alignment Scores:
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			Best Local Similarity:	Conservative: 0
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				Indels: 0
				Gaps: 0
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				BASE COUNT 140 a 157 c 167 g 159 t
				ORIGIN
				Alignment Scores:
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			Score:	Length: 110000
			Percent Similarity:	Matches: 25
			Best Local Similarity:	Conservative: 0
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				Gaps: 0
			US-09-895-298A-83 (1-190) x MMU297000 (1-623)	
				BASE COUNT 140 a 157 c 167 g 159 t
				ORIGIN
				Alignment Scores:
			Pred. No.:	25..9.89e-15
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				Indels: 0
				Gaps: 0
			US-09-895-298A-83 (1-190) x MMU297000 (1-623)	
				BASE COUNT 140 a 157 c 167 g 159 t
				ORIGIN
				Alignment Scores:
			Pred. No.:	25..9.89e-15
			Score:	Length: 110000
			Percent Similarity:	Matches: 25
			Best Local Similarity:	Conservative: 0
			Query	

Morbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Roselli,M., Roy,A., Santos,R., Schauer,S., Schupack,R., Seaman,S., Severy,P., Spencer,B., Stane-Thomann,N., Stojanovic,N., Straus,N., Subramanian,A., Talamas,J., Testafay,S., Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

JOURNAL

Submitted (23 NOV 2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

COMMENT

All repeats were identified using RepeatMasker:
Smit,A.F.A. & Green,P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Center: Whitehead Institute / MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu

Project Information

Center project name: Li3918
Center clone name: 35_B_17

NOTE: This record contains 87 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.

1 722: contig of 722 bp in length
* 723 822: gap of 100 bp
* 823 1526: contig of 704 bp in length
* 1527 1626: gap of 100 bp
* 1627 2336: contig of 710 bp in length
* 2337 2436: gap of 100 bp
* 2437 3156: contig of 720 bp in length
* 3157 3256: gap of 100 bp
* 3257 3984: contig of 728 bp in length
* 3985 4084: gap of 100 bp
* 4085 4811: contig of 727 bp in length
* 4812 4911: gap of 100 bp
* 4912 5638: contig of 727 bp in length
* 5639 5738: gap of 100 bp
* 5739 6477: contig of 739 bp in length
* 6478 6577: gap of 100 bp
* 6578 7305: contig of 728 bp in length
* 7306 7405: gap of 100 bp
* 7406 8107: contig of 702 bp in length
* 8108 8207: gap of 100 bp
* 8208 8950: contig of 743 bp in length
* 8951 9050: gap of 100 bp
* 9051 9743: contig of 693 bp in length
* 9744 9843: gap of 100 bp
* 9844 10583: contig of 740 bp in length
* 10584 11683: gap of 100 bp
* 10684 11405: contig of 722 bp in length
* 11406 11505: gap of 100 bp
* 11506 12216: contig of 731 bp in length
* 12237 12336: gap of 100 bp
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* 13070 13169: gap of 100 bp
* 13170 13851: contig of 682 bp in length
* 13852 13951: gap of 100 bp
* 13952 14685: contig of 734 bp in length
* 14686 14785: gap of 100 bp
* 14786 15512: contig of 727 bp in length
* 15513 15612: gap of 100 bp

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* 25428 26144: contig of 717 bp in length
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* 27078 27776: contig of 699 bp in length
* 27777 27876: gap of 100 bp
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* 28696 29420: contig of 725 bp in length
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* 31070 31165: gap of 100 bp
* 31170 31896: contig of 727 bp in length
* 31897 31996: gap of 100 bp
* 31997 32740: contig of 744 bp in length
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* 32841 33583: contig of 743 bp in length
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* 36066 36165: gap of 100 bp
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* 37795 38521: contig of 727 bp in length
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* 40191 40290: gap of 100 bp
* 40291 41012: contig of 722 bp in length
* 41013 41112: gap of 100 bp
* 41113 41852: contig of 740 bp in length
* 41853 41952: gap of 100 bp
* 41953 42686: contig of 736 bp in length
* 42689 42788: gap of 100 bp
* 42789 43523: contig of 735 bp in length
* 4324 43623: gap of 100 bp
* 4324 44118: contig of 695 bp in length
* 44319 44418: gap of 100 bp
* 44419 45138: contig of 720 bp in length
* 45139 45238: gap of 100 bp
* 45239 45976: contig of 738 bp in length

Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 8.42% Indels: 0
 DB: 6 Gaps: 0

US-09-895-298a-83 (1-190) x AX071021 (1-402)

QY 1 MetMetAsnPheGlnProProSerLysAlaPArgAlaSerGlnMet 16
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 269 ATGATGATTTCAGCTCCAGCAAGCCCTGGCGGCCACAGATG 316

Search completed: November 9, 2002, 08:33:48
 Job time : 2869 secs

Alignment Scores:
 Preド. No.: * 45977 46076: gap of 100 bp
 Score: * 46077 46088: contig of 732 bp in length
 Percent Similarity: * 46099 46908: gap of 100 bp
 Best Local Similarity: * 46909 46908: gap of 100 bp
 Query Match: * 47613: contig of 705 bp in length
 DB: * 47714 47713: gap of 100 bp
 * 48432 48531: contig of 718 bp in length
 * 48532 49280: contig of 100 bp
 * 49281 49380: gap of 100 bp
 * 49381 50139: contig of 759 bp in length
 * 50140 50239: gap of 100 bp
 * 50240 50366: contig of 727 bp in length
 * 50967 51066: gap of 100 bp
 * 51067 51797: contig of 731 bp in length
 * 51798 51897: gap of 100 bp
 * 51898 52032: contig of 735 bp in length
 * 52633 52732: gap of 100 bp
 * 52733 53448: contig of 716 bp in length
 * 53449 53548: gap of 100 bp
 * 53549 54266: contig of 718 bp in length
 * 54267 54366: gap of 100 bp
 * 54367 55107: contig of 741 bp in length
 * 55108 55207: gap of 100 bp
 * 55208 55327: contig of 720 bp in length
 * 55928 56027: gap of 100 bp
 * 56028 56757: contig of 730 bp in length
 * 56758 56857: gap of 100 bp

Length: 71596
 Matches: 17
 Conservative: 0
 Mismatches: 0
 Best Local Similarity: 100.00%
 Query Match: 8.95%
 DB: 2
 Gaps: 0

US-09-895-298a-83 (1-190) x AC100877 (1-71596)

QY 84 AsnLeuLeGlySerValHisPhePhePheLeuThrLeuLeuLeu 100
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 48783 ARCTCATGGAGTGTCACTCTCTCACCCTCATGGCTG 48833

RESULT 15

AX071021
 IACUS AX071021 402 bp DNA linear PAT 25-JAN-2001
 DEFINITION Sequence 1493 from Patent WO0102568.
 ACCESSION AX071021
 VERSION AX071021.1 GI:12581294

KEYWORDS
 SOURCE
 ORGANISM

Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarhini; Hominoidea; Homo.

REFERENCE
 1 (bases 1 to 402)

WILLIAMS,L.T., ESCOBEDO,J., INNIS,M.A., GARCIA,P.D., KLINGER,J.,

KASSAN,A., REINHARD,C., RANDAZZO,F., KENNEDY,G.C., POT,D., LAMSON,G., DRIMANAC,R., CRKENJAKOV,R., DRIMANAC,S., DICKSON,M., LABAT,I., LESHTOWITZ,D., KITA,D., GARCIA,V. AND STRACHE-CRAIN,B.

TITLE Human genes and gene expression products

JOURNAL Patent: WO 0102568 A 1493 11-JAN-2001;

CHIRON CORPORATION (US); HYSEQ, INC. (US)

FEATURES Location/Qualifiers

SOURCE

1. .402

/Organism="Homo sapiens"

/db_xref="Taxon:9606"

misc_feature 1. .402
 /note="n = A,T,C or G"
 /note="n = A,T,C or G"

BASE COUNT 83 a 106 c 87 g 124 t 2 others
 ORIGIN

Alignment Scores:
 Pred. No.: 2.75e-07 Length: 402
 Score: 16.00 Matches: 16

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